



SEQUENCE LISTING

<110> weigel, Paul H.

DeAngelis, Paul

Kumari, Kshama

<120> Hyaluronan Synthase Gene and Uses Thereof

<130> 3554.011

<140> US 09/469,200

<141> 1999-12-21

<150> US 09/178,851

<151> 1998-10-26

<150> US 60/064,435

<151> 1997-10-31

<160> 14

<170> PatentIn version 3.1

<210> 1

<211> 1254

<212> DNA

<213> Streptococcus equisimilis

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ctgatagctt acctattagt caaaatgtcc ttatcctttt tttacaagcc atttaaggga 180
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ttgctagaga cctaaaaag tggcgtcg	300
gttgcgtatg gaagtgtga tgagacagg	360
actggtacc tatcaagcaa tgtcattgtt catcggtcg	420
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gatgtttaa tgacccaact gttttgctg cgacgggtca	600
ccttaatgtc agaaatagac aaaccaatct cttaacacgc	660
ttgacagata ttgcgttatga taatgcttt ggcgttgaac	720
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gatacatcaa ccagaccttc ctgggtattc ctgttaagtat	900
tggtgatgac aggtgcttga ccaactatgc aactgattt	960
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<211> 417

<212> PRT

<213> Streptococcus Equisimilis

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Ser Leu Ser Ile Tyr Gly Phe Leu Leu Ile Ala Tyr Leu Leu Val Lys
 35 40 45

Met Ser Leu Ser Phe Phe Tyr Lys Pro Phe Lys Gly Arg Ala Gly Gln
 50 55 60

Tyr Lys Val Ala Ala Ile Ile Pro Ser Tyr Asn Glu Asp Ala Glu Ser
65 70 75 80

Leu Leu Glu Thr Leu Lys Ser Val Gln Gln Gln Thr Tyr Pro Leu Ala
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Glu Ile Tyr Val Val Asp Asp Gly Ser Ala Asp Glu Thr Gly Ile Lys
100 105 110

Arg Ile Glu Asp Tyr Val Arg Asp Thr Gly Asp Leu Ser Ser Asn Val
115 120 125

Ile Val His Arg Ser Glu Lys Asn Gln Gly Lys Arg His Ala Gln Ala
130 135 140

Trp Ala Phe Glu Arg Ser Asp Ala Asp Val Phe Leu Thr Val Asp Ser
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Asp Thr Tyr Ile Tyr Pro Asp Ala Leu Glu Glu Leu Leu Lys Thr Phe
165 170 175

Asn Asp Pro Thr Val Phe Ala Ala Thr Gly His Leu Asn Val Arg Asn
180 185 190

Arg Gln Thr Asn Leu Leu Thr Arg Leu Thr Asp Ile Arg Tyr Asp Asn
195 200 205

Ala Phe Gly Val Glu Arg Ala Ala Gln Ser Val Thr Gly Asn Ile Leu
210 215 220

Val Cys Ser Gly Pro Leu Ser Val Tyr Arg Arg Glu Val Val Val Pro
225 230 235 240

Asn Ile Asp Arg Tyr Ile Asn Gln Thr Phe Leu Gly Ile Pro Val Ser
245 250 255

Ile Gly Asp Asp Arg Cys Leu Thr Asn Tyr Ala Thr Asp Leu Gly Lys
260 265 270

Thr Val Tyr Gln Ser Thr Ala Lys Cys Ile Thr Asp Val Pro Asp Lys
275 280 285

Met Ser Thr Tyr Leu Lys Gln Gln Asn Arg Trp Asn Lys Ser Phe Phe
290 295 300

Arg Glu Ser Ile Ile Ser Val Lys Lys Ile Met Asn Asn Pro Phe Val
305 310 315 320

Ala Leu Trp Thr Ile Leu Glu Val Ser Met Phe Met Met Leu Val Tyr
325 330 335

Ser Val Val Asp Phe Phe Val Gly Asn Val Arg Glu Phe Asp Trp Leu
340 345 350

Arg Val Leu Ala Phe Leu Val Ile Ile Phe Ile Val Ala Leu Cys Arg
355 360 365

Asn Ile His Tyr Met Leu Lys His Pro Leu Ser Phe Leu Leu Ser Pro
370 375 380

Phe Tyr Gly Val Leu His Leu Phe Val Leu Gln Pro Leu Lys Leu Tyr
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<212> DNA

<213> Artificial Sequence

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<223> Primer se1

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<223> Primer sesp2
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<213> Paramecium bursaria chlorella virus

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<212> DNA

<213> *Pastuerella Multocida*

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<212> PRT

<213> *Pastuerella Multocida*

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 35 40 45

His Pro Ser Val Asn Ser Ala His Leu Ser Val Asn Lys Glu Glu Lys
 50 55 60

Val Asn Val Cys Asp Ser Pro Leu Asp Ile Ala Thr Gln Leu Leu Leu
 65 70 75 80

Ser Asn Val Lys Lys Leu Val Leu Ser Asp Ser Glu Lys Asn Thr Leu
 85 90 95

Lys Asn Lys Trp Lys Leu Leu Thr Glu Lys Lys Ser Glu Asn Ala Glu
 100 105 110

Val Arg Ala Val Ala Leu Val Pro Lys Asp Phe Pro Lys Asp Leu Val
115 120 125

Leu Ala Pro Leu Pro Asp His Val Asn Asp Phe Thr Trp Tyr Lys Lys
130 135 140

Arg Lys Lys Arg Leu Gly Ile Lys Pro Glu His Gln His Val Gly Leu
145 150 155 160

Ser Ile Ile Val Thr Thr Phe Asn Arg Pro Ala Ile Leu Ser Ile Thr
165 170 175

Leu Ala Cys Leu Val Asn Gln Lys Thr His Tyr Pro Phe Glu Val Ile
180 185 190

Val Thr Asp Asp Gly Ser Gln Glu Asp Leu Ser Pro Ile Ile Arg Gln
195 200 205

Tyr Glu Asn Lys Leu Asp Ile Arg Tyr Val Arg Gln Lys Asp Asn Gly
210 215 220

Phe Gln Ala Ser Ala Ala Arg Asn Met Gly Leu Arg Leu Ala Lys Tyr
225 230 235 240

Asp Phe Ile Gly Leu Leu Asp Cys Asp Met Ala Pro Asn Pro Leu Trp
245 250 255

Val His Ser Tyr Val Ala Glu Leu Leu Glu Asp Asp Asp Leu Thr Ile
260 265 270

Ile Gly Pro Arg Lys Tyr Ile Asp Thr Gln His Ile Asp Pro Lys Asp
275 280 285

Phe Leu Asn Asn Ala Ser Leu Leu Glu Ser Leu Pro Glu Val Lys Thr
290 295 300

Asn Asn Ser Val Ala Ala Lys Gly Glu Gly Thr Val Ser Leu Asp Trp
305 310 315 320

Arg Leu Glu Gln Phe Glu Lys Thr Glu Asn Leu Arg Leu Ser Asp Ser
325 330 335

Pro Phe Arg Phe Phe Ala Ala Gly Asn Val Ala Phe Ala Lys Lys Trp
340 345 350

Leu Asn Lys Ser Gly Phe Phe Asp Glu Glu Phe Asn His Trp Gly Gly
355 360 365

Glu Asp Val Glu Phe Gly Tyr Arg Leu Phe Arg Tyr Gly Ser Phe Phe
370 375 380

Lys Thr Ile Asp Gly Ile Met Ala Tyr His Gln Glu Pro Pro Gly Lys
385 390 395 400

Glu Asn Glu Thr Asp Arg Glu Ala Gly Lys Asn Ile Thr Leu Asp Ile
405 410 415

Met Arg Glu Lys Val Pro Tyr Ile Tyr Arg Lys Leu Leu Pro Ile Glu
420 425 430

Asp Ser His Ile Asn Arg Val Pro Leu Val Ser Ile Tyr Ile Pro Ala
435 440 445

Tyr Asn Cys Ala Asn Tyr Ile Gln Arg Cys Val Asp Ser Ala Leu Asn
450 455 460

Gln Thr Val Val Asp Leu Glu Val Cys Ile Cys Asn Asp Gly Ser Thr
465 470 475 480

Asp Asn Thr Leu Glu Val Ile Asn Lys Leu Tyr Gly Asn Asn Pro Arg
485 490 495

Val Arg Ile Met Ser Lys Pro Asn Gly Gly Ile Ala Ser Ala Ser Asn
500 505 510

Ala Ala Val Ser Phe Ala Lys Gly Tyr Tyr Ile Gly Gln Leu Asp Ser
515 520 525

Asp Asp Tyr Leu Glu Pro Asp Ala Val Glu Leu Cys Leu Lys Glu Phe
530 535 540

Leu Lys Asp Lys Thr Leu Ala Cys Val Tyr Thr Thr Asn Arg Asn Val
545 550 555 560

Asn Pro Asp Gly Ser Leu Ile Ala Asn Gly Tyr Asn Trp Pro Glu Phe
565 570 575

Ser Arg Glu Lys Leu Thr Thr Ala Met Ile Ala His His Phe Arg Met
580 585 590

Phe Thr Ile Arg Ala Trp His Leu Thr Asp Gly Phe Asn Glu Lys Ile
595 600 605

Glu Asn Ala Val Asp Tyr Asp Met Phe Leu Lys Leu Ser Glu Val Gly
610 615 620

Lys Phe Lys His Leu Asn Lys Ile Cys Tyr Asn Arg Val Leu His Gly
625 630 635 640

Asp Asn Thr Ser Ile Lys Lys Leu Gly Ile Gln Lys Lys Asn His Phe
645 650 655

Val Val Val Asn Gln Ser Leu Asn Arg Gln Gly Ile Thr Tyr Tyr Asn
660 665 670

Tyr Asp Glu Phe Asp Asp Leu Asp Glu Ser Arg Lys Tyr Ile Phe Asn
675 680 685

Lys Thr Ala Glu Tyr Gln Glu Glu Ile Asp Ile Leu Lys Asp Ile Lys
690 695 700

Ile Ile Gln Asn Lys Asp Ala Lys Ile Ala Val Ser Ile Phe Tyr Pro
705 710 715 720

Asn Thr Leu Asn Gly Leu Val Lys Lys Leu Asn Asn Ile Ile Glu Tyr
725 730 735

Asn Lys Asn Ile Phe Val Ile Val Leu His Val Asp Lys Asn His Leu
740 745 750

Thr Pro Asp Ile Lys Lys Glu Ile Leu Ala Phe Tyr His Lys His Gln
755 760 765

Val Asn Ile Leu Leu Asn Asn Asp Ile Ser Tyr Tyr Thr Ser Asn Arg
770 775 780

Leu Ile Lys Thr Glu Ala His Leu Ser Asn Ile Asn Lys Leu Ser Gln
785 790 795 800

Leu Asn Leu Asn Cys Glu Tyr Ile Ile Phe Asp Asn His Asp Ser Leu
805 810 815

Phe Val Lys Asn Asp Ser Tyr Ala Tyr Met Lys Lys Tyr Asp Val Gly
820 825 830

Met Asn Phe Ser Ala Leu Thr His Asp Trp Ile Glu Lys Ile Asn Ala
835 840 845

His Pro Pro Phe Lys Lys Leu Ile Lys Thr Tyr Phe Asn Asp Asn Asp
850 855 860

Leu Lys Ser Met Asn Val Lys Gly Ala Ser Gln Gly Met Phe Met Thr
865 870 875 880

Tyr Ala Leu Ala His Glu Leu Leu Thr Ile Ile Lys Glu Val Ile Thr
885 890 895

Ser Cys Gln Ser Ile Asp Ser Val Pro Glu Tyr Asn Thr Glu Asp Ile
900 905 910

Trp Phe Gln Phe Ala Leu Leu Ile Leu Glu Lys Lys Thr Gly His Val
915 920 925

Phe Asn Lys Thr Ser Thr Leu Thr Tyr Met Pro Trp Glu Arg Lys Leu
930 935 940

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<213> Paramecium bursaria chorella virus

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Gly Val Ser Ala Tyr Gly Ile Phe Val Phe Gly Phe Phe Leu Ala Gln
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Val Leu Phe Ser Glu Leu Asn Arg Lys Arg Leu Arg Lys Trp Ile Ser
65 70 75 80

Leu Arg Pro Lys Gly Trp Asn Asp Val Arg Leu Ala Val Ile Ile Ala
85 90 95

Gly Tyr Arg Glu Asp Pro Tyr Met Phe Gln Lys Cys Leu Glu Ser Val
100 105 110

Arg Asp Ser Asp Tyr Gly Asn Val Ala Arg Leu Ile Cys Val Ile Asp
115 120 125

Gly Asp Glu Asp Asp Asp Met Arg Met Ala Ala Val Tyr Lys Ala Ile
130 135 140

Tyr Asn Asp Asn Ile Lys Lys Pro Glu Phe Val Leu Cys Glu Ser Asp
145 150 155 160

Asp Lys Glu Gly Glu Arg Ile Asp Ser Asp Phe Ser Arg Asp Ile Cys
165 170 175

Val Leu Gln Pro His Arg Gly Lys Arg Glu Cys Leu Tyr Thr Gly Phe
180 185 190

Gln Leu Ala Lys Met Asp Pro Ser Val Asn Ala Val Val Leu Ile Asp
195 200 205

Ser Asp Thr Val Leu Glu Lys Asp Ala Ile Leu Glu Val Val Tyr Pro
210 215 220

Leu Ala Cys Asp Pro Glu Ile Gln Ala Val Ala Gly Glu Cys Lys Ile
225 230 235 240

Trp Asn Thr Asp Thr Leu Leu Ser Leu Leu Val Ala Trp Arg Tyr Tyr
245 250 255

Ser Ala Phe Cys Val Glu Arg Ser Ala Gln Ser Phe Phe Arg Thr Val
260 265 270

Gln Cys Val Gly Gly Pro Leu Gly Ala Tyr Lys Ile Asp Ile Ile Lys
275 280 285

Glu Ile Lys Asp Pro Trp Ile Ser Gln Arg Phe Leu Gly Gln Lys Cys
290 295 300

Thr Tyr Gly Asp Asp Arg Arg Leu Thr Asn Glu Ile Leu Met Arg Gly
305 310 315 320

Lys Lys Val Val Phe Thr Pro Phe Ala Val Gly Trp Ser Asp Ser Pro
325 330 335

Thr Asn Val Phe Arg Tyr Ile Val Gln Gln Thr Arg Trp Ser Lys Ser
340 345 350

Trp Cys Arg Glu Ile Trp Tyr Thr Leu Phe Ala Ala Trp Lys His Gly
355 360 365

Leu Ser Gly Ile Trp Leu Ala Phe Glu Cys Leu Tyr Gln Ile Thr Tyr
370 375 380

Phe Phe Leu Val Ile Tyr Leu Phe Ser Arg Leu Ala Val Glu Ala Asp
385 390 395 400

Pro Arg Ala Gln Thr Ala Thr Val Ile Val Ser Thr Thr Val Ala Leu
405 410 415

Ile Lys Cys Gly Tyr Phe Ser Phe Arg Ala Lys Asp Ile Arg Ala Phe
420 425 430

Tyr Phe Val Leu Tyr Thr Phe Val Tyr Phe Phe Cys Met Ile Pro Ala
435 440 445

Arg Ile Thr Ala Met Met Thr Leu Trp Asp Ile Gly Trp Gly Thr Arg
450 455 460

Gly Gly Asn Glu Lys Pro Ser Val Gly Thr Arg Val Ala Leu Trp Ala
465 470 475 480

Lys Gln Tyr Leu Ile Ala Tyr Met Trp Trp Ala Ala Val Val Gly Ala
485 490 495

Gly Val Tyr Ser Ile Val His Asn Trp Met Phe Asp Trp Asn Ser Leu
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Ser Tyr Arg Phe Ala Leu Val Gly Ile Cys Ser Tyr Ile Val Phe Ile
515 520 525

Val Ile Val Leu Val Val Tyr Phe Thr Gly Lys Ile Thr Thr Trp Asn
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<212> PRT

<213> Streptococcus pyogenes

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<212> DNA

<213> artificial sequence

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